



SEQUENCE LISTING

<110> LEWIN, DAVID A.
PENNICA, DIANE
RASTELLI, LUCA
TALLION, BRUCE

<120> WNT-REGULATED CYTOKINE-LIKE POLYPEPTIDE AND NUCLEIC ACIDS ENCODING SAME

<130> 11669.191USU1

<140> 09/715,418
<141> 2000-11-16

<150> 60/166,177
<151> 1999-11-18

<160> 49

<170> PatentIn Ver. 2.1

<210> 1
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<212> DNA
<213> Mus sp.

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tgtaatgact cgaaaacttggaa gtttggaaac tt 212

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<213> Mus sp.

<220>
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<222> (1541)
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ctcacagaag gaaggaccag tgtaccagga acgtgggac agtgtcggtc agccaatgct 180
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cataaaatact ctgtggcggtt taaaaaggaa acactgaccc ctgctgagct tcgagacctg 300
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gaagcagccca agagtgtgaa gatggagagg cctgttactc ggagctgagg acttctactt 480
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<210> 3
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<400> 3
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 Leu Thr Glu Gly Arg Thr Ser Val Pro Gly Thr Met Gly Gln Cys Arg
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 Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser Asp Val Glu Arg Ala
 35 40 45

 Ile Glu Thr Leu Ile Lys Asn Phe His Lys Tyr Ser Val Ala Gly Lys
 50 55 60

 Lys Glu Thr Leu Thr Pro Ala Glu Leu Arg Asp Leu Val Thr Gln Gln
 65 70 75 80

 Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu Glu Glu Lys Ile Ala
 85 90 95

 Asn Leu Gly Asn Cys Asn Asp Ser Lys Leu Glu Phe Gly Ser Phe Trp
 100 105 110

 Glu Leu Ile Gly Glu Ala Ala Lys Ser Val Lys Met Glu Arg Pro Val
 115 120 125

 Thr Arg Ser
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<210> 4
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 <212> DNA

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<213> Homo sapiens

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<222> (337)
<223> "n" represents a, t, c, g, other or unknown

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gctacgggac ctggtcaccc agcagctgcc ccacatctcatg ccgagcaact ntggcctgga 240
agagaaaatt gccaacctgg gcagctgaa tgactctaaa ctggagttca ggagtttctg 300
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<213> Homo sapiens

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ggtagccagg tcccgtagct cagaaggggt cagcgtctcc ttcccaccct ccacggagta 240
ctggtaaaag ttcttgatga gggtctcaat ggcctctcc acatcaactga attcctgagc 300
atccctctgcg ttggctgacc gacactgtcc catggtgctc actgtgtctg gtccttttgt 360
gagagttctg ttgtccat 379

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<211> 118
<212> PRT
<213> Homo sapiens

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Asp Asn Arg Thr Leu Thr Lys Gly Pro Asp Thr Val Ser Thr Met Gly
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Gln Cys Arg Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser Asp Val
 20          25          30

Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr Ser Val
 35          40          45

Glu Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp Leu Val
 50          55          60

Thr Gln Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu Glu Glu
 65          70          75          80

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Lys Ile Ala Asn Leu Gly Ser Cys Asn Asp Ser Lys Leu Glu Phe Arg
85 90 95
Ser Phe Trp Glu Leu Ile Gly Glu Ala Ala Lys Ser Val Lys Leu Glu
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Arg Pro Val Arg Gly His
115

<210> 7
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 7
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<210> 8
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe

<400> 8
ccacatcaact gaattcctga gcatcc 26

<210> 9
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 9
cagacacagt gagcaccatg 20

<210> 10
<211> 98
<212> PRT
<213> Homo sapiens, W27152, chemotactic cytokine II CCII from WO97/34013

<400> 10
Met Ala Ala Glu Pro Leu Thr Glu Leu Glu Ser Ile Glu Thr Val
1 5 10 15

Val Thr Thr Phe Phe Thr Phe Ala Arg Gln Glu Gly Arg Lys Asp Ser
20 25 30

Leu Ser Val Asn Glu Phe Lys Glu Leu Val Thr Gln Gln Leu Pro His
35 40 45

Leu Leu Lys Asp Val Gly Ser Leu Asp Glu Lys Met Lys Ser Leu Asp
50 55 60

Val Asn Gln Asp Ser Glu Leu Lys Phe Asn Glu Tyr Trp Arg Leu Ile
65 70 75 80

Gly Glu Leu Ala Lys Glu Ile Arg Lys Lys Lys Asp Leu Lys Ile Arg
85 90 95

Lys Lys

<210> 11
<211> 110
<212> PRT
<213> Homo sapiens, G491246, Macrophage Migration Inhibition Factor (MRP-14)

<400> 11
Met Ser Gln Leu Glu Arg Asn Ile Glu Thr Ile Ile Asn Thr Phe His
1 5 10 15

Gln Tyr Ser Val Lys Leu Gly His Pro Asp Thr Leu Asn Gln Gly Glu
20 25 30

Phe Lys Glu Leu Val Arg Lys Asp Leu Gln Asn Phe Leu Lys Lys Glu
35 40 45

Asn Lys Asn Glu Lys Val Ile Glu His Ile Met Glu Asp Leu Asp Thr
50 55 60

Asn Ala Asp Lys Gln Leu Ser Phe Glu Glu Phe Ile Met Leu Met Ala
65 70 75 80

Arg Leu Thr Trp Ala Ser His Glu Lys Met His Glu Gly Asp Glu Gly
85 90 95

Pro Gly His His Lys Pro Gly Leu Gly Glu Gly Thr Pro
100 105 110

<210> 12
<211> 37
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: 3-100/ICaBP type
calcium binding protein

<400> 12
Ser Asn Cys Gly Leu Glu Glu Lys Ile Ala Asn Leu Gly Ser Cys Asn
1 5 10 15

Asp Ser Lys Leu Glu Phe Arg Ser Phe Trp Glu Leu Ile Gly Glu Ala
20 25 30

Ala Lys Ser Val Lys
35

<210> 13
<211> 37
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: 3-100/ICaBP type
calcium binding protein

<400> 13
Asp Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr
1 5 10 15

Ser Val Glu Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp
20 25 30

Leu Val Thr Gln Gln
35

<210> 14
<211> 19
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Bacterial type II
secretion system protein F

<400> 14
Val Thr Gln Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu Glu
1 5 10 15

Glu Lys Ile

<210> 15
<211> 10
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Ubiquitin
carboxyl-terminal hydrolases family

<400> 15
Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser
1 5 10

<210> 16
<211> 49
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Bacterial
themotaxis sensory transducers protein

<400> 16
Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp Leu Val Thr
1 5 10 15

Gln Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu Glu Glu Lys
20 25 30

Ile Ala Asn Leu Gly Ser Cys Asn Asp Ser Lys Leu Glu Phe Arg Ser
35 40 45

Phe

<210> 17
<211> 32
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism:
Phosphoenolpyruvate carboxykinase (ATP) protein

<400> 17
Met Gly Gln Cys Arg Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser
1 5 10 15

Asp Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr
20 25 30

<210> 18
<211> 33
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Prokaryotic-type
carbonic anhydrases proteins

<400> 18

His Gln Tyr Ser Val Glu Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu
1 5 10 15

Leu Arg Asp Leu Val Thr Gln Gln Leu Pro His Leu Met Pro Ser Asn
20 25 30

Cys

<210> 19
<211> 15
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Ergosterol
biosynthesis ERG4/ERG24 family protein

<400> 19
Ile Ala Asn Leu Gly Ser Cys Asn Asp Ser Lys Leu Glu Phe Arg
1 5 10 15

<210> 20
<211> 25
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism:
Lysosome-associated membrane glycoproteins du

<400> 20
Leu Met Pro Ser Asn Cys Gly Leu Glu Glu Lys Ile Ala Asn Leu Gly
1 5 10 15

Ser Cys Asn Asp Ser Lys Ile Glu Phe
20 25

<210> 21
<211> 39
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism:
Phosphofructokinase proteins

<400> 21
Pro Ser Asn Cys Gly Leu Glu Glu Lys Ile Ala Asn Leu Gly Ser Cys
1 5 10 15

Asn Asp Ser Lys Leu Glu Phe Arg Ser Phe Trp Glu Leu Ile Gly Glu
20 25 30

Ala Ala Lys Ser Val Lys Leu
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<210> 22
<211> 10
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: PH domain
proteins profile

<400> 22
Pro Ser Asn Cys Gly Leu Glu Glu Lys Ile
1 5 10

<210> 23
<211> 45
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Myotoxins
protein

<400> 23
Gln Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu Glu Glu Lys
1 5 10 15

Ile Ala Asn Leu Gly Ser Cys Asn Asp Ser Lys Leu Glu Phe Arg Ser
20 25 30

Phe Trp Glu Leu Ile Gly Glu Ala Ala Lys Ser Val Lys
35 40 45

<210> 24
<211> 17
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism:
Phosphatidylinositol-specific phospholipase X

<400> 24
Met Pro Ser Asn Cys Gly Leu Glu Glu Lys Ile Ala Asn Leu Gly Ser
1 5 10 15

Cys

<210> 25
<211> 45

<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Glypicans protein

<400> 25
Met Gly Gly Cys Arg Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser
1 5 10 15

Asp Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr
20 25 30

Ser Val Glu Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu
35 40 45

<210> 26
<211> 10
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Membrane attack complex components/perforin

<400> 26
Ile Lys Asn Phe His Gln Tyr Ser Val Glu
1 5 10

<210> 27
<211> 44
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Urease nickel ligands protein

<400> 27
Thr Leu Ile Lys Asn Phe His Gln Tyr Ser Val Glu Gly Gly Lys Glu
1 5 10 15

Thr Leu Thr Pro Ser Glu Leu Arg Asp Leu Val Thr Gln Gln Leu Pro
20 25 30

His Leu Met Pro Ser Asn Cys Gly Leu Glu Glu Lys
35 40

<210> 28
<211> 13
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Phosphoglycerate
mutase family phosphohistidi

<400> 28
Gln Glu Phe Ser Asp Val Glu Arg Ala Ile Glu Thr Leu
1 5 10

<210> 29
<211> 10
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Ribosomal protein
L23 protein

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Glu Leu Arg Asp Leu Val Thr Gln Gln Leu
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<210> 30
<211> 41
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism:
2'-5'-oligoadenylate synthetases protein

<400> 30
Leu Glu Glu Lys Ile Ala Asn Leu Gly Ser Cys Asn Asp Ser Lys Leu
1 5 10 15

Glu Phe Arg Ser Phe Trp Glu Leu Ile Gly Glu Ala Ala Lys Ser Val
20 25 30

Lys Leu Glu Arg Pro Val Arg Gly His
35 40

<210> 31
<211> 24
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Formate and
nitrite transporters protein

<400> 31
Asp Leu Val Thr Gln Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly
1 5 10 15

Leu Glu Glu Lys Ile Ala Asn Leu
20

<210> 32
<211> 34
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Glycoprotein
hormones beta chain protein

<400> 32
Gly Gln Cys Arg Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser Asp
1 5 10 15

Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr Ser
20 25 30

Val Glu

<210> 33
<211> 21
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Vinculin family
talin-binding region protein

<400> 33
Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp Leu Val Thr Gln Gln
1 5 10 15

Leu Pro His Leu Met
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<210> 34
<211> 40
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Beta-lactamases
clas B protein

<400> 34
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1 5 10 15

Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp Leu Val Thr Gln Gln
12

20

25

30

Leu Pro His Leu Met Pro Ser Asn
35 40

<210> 35
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<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Heat shock hsp20
protein family profile

<400> 35
Leu Glu Phe Arg Ser Phe Trp Glu Leu Ile Gly Glu Ala Ala Lys Ser
1 5 10 15

Val Lys Leu Glu Arg
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<210> 36
<211> 35
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism:
Hydroxymethylglutaryl-coenzyme A lyase protein

<400> 36
Met Gly Gly Cys Arg Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser
1 5 10 15

Asp Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr
20 25 30

Ser Val Glu
35

<210> 37
<211> 294
<212> DNA
<213> Mus sp.

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<210> 38
 <211> 43
 <212> PRT
 <213> Homo sapiens

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Val Glu Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp Leu
 20 25 30

Val Thr Gln Gln Leu Pro His Leu Met Pro Ser
 35 40

<210> 39
 <211> 104
 <212> PRT
 <213> Homo sapiens translation of GenBank Accession AAY007220

<400> 39

Met Gly Gln Cys Arg Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser
 1 5 10 15

Asp Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr
 20 25 30

Ser Val Glu Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp
 35 40 45

Leu Val Thr Gln Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu
 50 55 60

Glu Glu Lys Ile Ala Asn Leu Gly Ser Cys Asn Asp Ser Lys Leu Glu
 65 70 75 80

Phe Arg Ser Phe Trp Glu Leu Ile Gly Glu Ala Ala Lys Ser Val Lys
 85 90 95

Leu Glu Arg Pro Val Arg Gly His
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<210> 40
 <211> 94
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Consensus sequence

<400> 40

Met Gly Gln Cys Arg Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser
1 5 10 15

Asp Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Tyr Ser
20 25 30

Val Gly Lys Glu Thr Leu Thr Pro Glu Leu Arg Asp Leu Val Thr Gln
35 40 45

Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu Glu Glu Lys Ile
50 55 60

Ala Asn Leu Gly Cys Asn Asp Ser Lys Leu Glu Phe Ser Phe Trp Glu
65 70 75 80

Leu Ile Gly Glu Ala Ala Lys Ser Val Lys Glu Arg Pro Val
85 90

<210> 41
<211> 41
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: gi/4139958/pdb/1MHO

<400> 41
Glu Lys Ala Val Val Ala Leu Ile Asp Val Phe His Gln Tyr Ser Gly
1 5 10 15

Arg Glu Gly Asp Lys His Lys Leu Lys Lys Ser Glu Leu Lys Glu Leu
20 25 30

Ile Asn Asn Glu Leu Ser His Phe Leu
35 40

<210> 42
<211> 41
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Protein MRP-126

<400> 42
Glu Lys Ala Ile Asp Val Ile Ile Asp Val Phe His Gln Tyr Ser Arg
1 5 10 15

Arg Glu Gly Asp Lys Asp Thr Leu Thr Arg Lys Glu Leu Lys Leu Leu
20 25 30

Ile Glu Lys Gln Leu Ala Asn Tyr Leu
35 40

<210> 43
<211> 41
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: ICTACALCIN

<400> 43
Gln Lys Gly Met Ala Leu Leu Ile Ser Thr Phe His Tyr Ser Gly
1 5 10 15

Lys Glu Gly Asp Lys Cys Thr Leu Thr Lys Gly Glu Leu Lys Asp Leu
20 25 30

Ile Thr Lys Glu Leu Gly Gly Ala Phe
35 40

<210> 44
<211> 41
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: CALGRANULIN B

<400> 44
Glu Ser Ser Ile Glu Thr Ile Ile Asn Ile Phe His Gln Tyr Ser Val
1 5 10 15

Arg Leu Gly His Tyr Asp Thr Leu Ile Gln Lys Glu Phe Lys Gln Leu
20 25 30

Val Gln Lys Glu Leu Pro Asn Phe Leu
35 40

<210> 45
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus sequence

<400> 45
Ile Phe His Tyr Ser Gly Leu Glu Leu Leu
1 5 10

<210> 46
<211> 41
<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: CALGRANULIN B

<400> 46

Glu Arg Ser Ile Thr Thr Ile Ile Asp Thr Phe His Gln Tyr Ser Arg
1 5 10 15

Lys Glu Gly His Pro Asp Thr Leu Ser Lys Lys Glu Phe Arg Gln Met
20 25 30

Val Glu Ala Gln Leu Ala Thr Phe Met
35 40

<210> 47

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus sequence

<400> 47

Glu Ile Phe His Gln Tyr Ser Gly Leu Glu Leu
1 5 10

<210> 48

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Unknown Organism: reverse strand sequence of SEQ ID NO:4 (GenBank AA315020)

<220>

<221> misc_feature

<222> (21)..(21)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (127)..(127)

<223> n is a, c, g, or t

<400> 48

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aggccanagt tgctcgcat gagatggggc agctgctggg tgaccaggtc ccgtagctca 180
gaaggggtca gcgtctcctt cccaccctcc acggagtaat ggtgaaagt cttgatgagg 240
gtctcaatgg ccctctccac atcactgaat tcctgagcat cctctgcgtt ggctgaccga 300
cactgtccca tggtgctcac tgtgtctggt cctttggtga gagttctgtt gccttat 357

<210> 49
<211> 104
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus
sequence

<400> 49
Met Gly Gln Cys Arg Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser
1 5 10 15

Asp Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr
20 25 30

Ser Val Glu Gly Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp
35 40 45

Leu Val Thr Gln Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu
50 55 60

Glu Glu Lys Ile Ala Asn Leu Gly Ser Cys Asn Asp Ser Lys Leu Glu
65 70 75 80

Phe Arg Ser Phe Trp Glu Leu Ile Gly Glu Ala Ala Lys Ser Val Lys
85 90 95

Leu Glu Arg Pro Val Arg Gly His
100